Amendments to the Specification:

Please replace the first full paragraph on page 2 with the following paragraph:

The global analysis of cellular proteins has recently been termed proteomics and is a key area of research that is developing in the post-genome era. Proteomics uses a combination of sophisticated techniques including two-dimensional (2D) gel electrophoresis, image analysis, mass spectrometry, amino acid sequencing, and bio-informatics to resolve comprehensively, to quantify, and to characterize proteins (for reviews, see Chambers G et al. „"Proteomics: a new approach to the study of disease"" J Pathol 2000 Nov;192(3):280-8; Banks RE et al. „"Proteomics: new perspectives, new biomedical opportunities"" Lancet 2000 Nov 18;356(9243):1749-56).

Please replace the paragraph bridging pages 2 and 3 with the following paragraph:

Proteomics is further said to contribute greatly to the understanding of gene function in the post-genomic era. Proteomics can be divided into three main areas: (1) protein micro-characterization for large-scale identification of proteins and their post-translational modifications; (2) 'differential display' proteomics for comparison of protein levels with potential application in a wide range of diseases; and (3) studies of protein-protein interactions using techniques such as mass spectrometry or the yeast two-hybrid system. Because it is often difficult to predict the function of a protein based on homology to other proteins or even their three-dimensional structure, determination of the components of a protein complex or of a cellular structure is central in functional analysis (Pandey A et al. „"Proteomics to study genes and genomes."" Nature 2000 Jun 15;405(6788):837-46).

Please replace the first full paragraph on page 3 with the following paragraph:

Due to the complexity of higher eukaryotic cells, single-step characterization of a proteome is likely to be difficult to achieve. Jung et al. („"Proteomics meets cell biology: the establishment of subcellular proteomes"" Electrophoresis 2000 Oct;21(16):3369-77) describe, that advantage can be taken of the macromolecular architecture of a cell, e.g., subcellular compartments, organelles, macromolecular structures and multiprotein complexes, to establish subcellular proteomes.

Please replace the paragraph bridging pages 4 and 5 with the following paragraph:

Sturtevant et al. („"Applications of differential-display reverse transcription-PCR to molecular pathogenesis and medical mycology." Clin Microbiol Rev 2000 Jul;13(3):408-27) describe the characterisation of host-fungus interactions by changes in gene expression in both host and pathogen. Differential-display reverse transcription PCR (DDRT-PCR) is a PCR-based method that allows extensive analysis of gene expression among several cell populations. DDRT-PCR has been used to address biological questions in mammalian systems, including cell differentiation, cell activation, cell stress, and identification of drug targets. In microbial pathogenesis and plant pathogenesis, DDRT-PCR has allowed the identification of virulence factors, genes involved in cell death, and signaling genes. Further, To („"Identification of differential gene expression by high throughput analysis"" Comb Chem High Throughput Screen 2000 Jun;3(3):235-41) describes the high throughput analysis of differential gene expression as a powerful tool that can be applied to many areas in molecular cell biology, including differentiation, development, physiology, and pharmacology. In recent years, a variety of techniques have been developed to analyze differential gene expression, including comparative expressed sequence tag sequencing,

differential display, representational difference analysis, cDNA or oligonucleotide arrays, and serial analysis of gene expression. Similar strategies are described by Oetting („"Gene expression analysis." Pigment Cell Res 2000 Feb;13(1):21-7) and Watson („"Differential cDNA screening strategies to identify novel stage-specific proteins in the developing mammalian brain." Dev Neurosci 1993;15(2):77-86).

Please replace the paragraph bridging pages 20 and 21 with the following paragraph:

Celis et al. („"Gene expression profiling: monitoring transcription and translation products using DNA microarrays and proteomics"" FEBS Lett 2000 Aug 25;480(1):2-16) describe a theoretical approach to combining different technologies such as DNA microarrays and proteomics, which have made possible the analysis of the expression levels of multiple genes simultaneously both in health and disease. In combination, these technologies are said to revolutionise biology, in particular in the area of molecular medicine as they are expected to reveal gene regulation events involved in disease progression as well as to pinpoint potential targets for drug discovery and diagnostics. Celis et al. review the current status of these technologies and highlight some studies in which they have been applied in concert to the analysis of biopsy specimens. Nevertheless, Celis et al. fail to describe or propose the combination of, in particular, data obtained in proteomics expression studies and methylation analyses in order to provide gene panels for further therapeutic or diagnostic purposes.

Please replace the first paragraph on page 25 with the following paragraph:

In another preferred method according to the invention, the selection is performed in such a way as to give a first knowledge base comprising only one set of selected genes. Thus, the knowledge base will comprise only „"on"" and „"off"" type of

data which allows for a very simple decision between expressed or non-expressed genes. In yet another embodiment of the inventive method, the selection is performed in such a way as to give a first knowledge base comprising different subsets of selected genes. Such classes can be referred to as „quality classes" which allows for a much more differentiated selection of the gene panel. The term „quality classes" as used herein comprises all different possibilities of groupings the different expression levels. Such grouping could, for example, include different importance for the selected sites for the analysis of the expression as well as statistical preciseness and/or quality of the analysis data of the selected gene.

Please replace the paragraph bridging pages 26 and 27 with the following paragraph:

In another embodiment of the method according to the invention, the analysis of the level of cytosine methylation comprises chemical treatment with bisulphite, hydrogen sulphite or disulphite, polymerase chain reaction (PCR), hybridisation analyses, sequencing, mass spectrometry and fluorescent, enzymatic, radioactive, dye and/or antibody labelling. In general, all methods for the analysis of the methylation statuses at selected sites of the DNA can be employed. Such methods are known to the skilled artisan and are described in, for example, Dahl et al., „Analysis of in vivo methylation." Methods Mol Biol 2000;130:47-57; Zhou Y. et al., „Use of a single sequencing termination reaction to distinguish between cytosine and 5-methylcytosine in bisulfite-modified DNA." Biotechniques 1997 May;22(5):850-4; Yoder JA et al. „Genetic analysis of genomic methylation patterns in plants and mammals." C Biol Chem 1996 Oct;377(10):605-10 and others.

Please replace the second full paragraph on page 27 with the following paragraph:

Another preferred method according to the invention is characterised in that all potentially methylated sites of the DNA are analysed. Such sites usually include all so-called „"CpG"-islands on a given DNA sequence and are readily detectable by the person skilled in the art. Preferably, the level of cytosine methylation of at least two genes are analysed in parallel. Preferably, the level of at least 100 cytosine methylation sites is analysed in parallel. The analysis of a multitude of sites in parallel allows for both a effective screening and a statistically highly relevant result of the method.

Please replace the paragraph bridging pages 27 and 28 with the following paragraph:

A further preferred method according to the invention is characterised in that the selection is based on the result of at least two individual rows of analyses. This will reduce the statistical error for the value of the methylation sensitivity of a selected site with an only limited increase of the costs for the analysis. In another preferred method according to the invention, the selection is performed in such a way to give a second knowledge base comprising only one set of selected genes. Thus, the knowledge base will comprise only „"on"" and „"off"" type of data which allows for a very simple decision between different methylation states.

Please replace the first full paragraph on page 28 with the following paragraph:

In yet another embodiment of the inventive method, the selection is performed in such a way to give a second knowledge base comprising different subsets of selected genes. Such classes can be referred to as „"quality classes"" which allows for a much more differentiated analysis.

Please replace the paragraph bridging pages 29 and 30 with the following paragraph:

Another embodiment of the method according to the invention is characterised in that steps a) to f) are repeated. Repeating the method of the invention suits several different purposes. First, as mentioned above, the statistical quality of the of the resulting data increases. Second, an internal control can be provided, whether the biological sample was taken correctly and resembles e.g. the tissue of interest. The number of repeating „"cycles"" of the invention can vary depending on the individual case, e.g. depending on the quality of the sample to be analyse. One possibility would be to repeat the method of the invention for at least 5 to 50 times. Preferably, such method according to the invention is characterised in that the method is at least partially performed by means of a suited automate, for example a robot and/or a computer system. The inventive method can be conveniently automated and/or computerized and respective devices and programs are readily known to the person skilled in the art.

Please replace the paragraph bridging pages 31 and 32 with the following paragraph:

According to the present invention, a „"gene panel"" designates a knowledge base, listing, table or other information source, that contains information about selected genes, herein also designated as „"candidate genes"". According to the present invention, the term „"gene panel"" should not be understood as merely containing information about the names or designations of the candidate genes. The panel further can contain additional information about the candidate genes, like sequence data, information about the origin (heredity) of the gene, species information, and information about the genetic elements and/or factors that influence expression of the candidate

gene(s). Such elements can be the complete genes and/or promoters, introns, first exons and/or enhancers of the candidate genes. Factors can be growth conditions, developmental stage of the biological material from which the candidate gene is derived or other medical data.

Please replace the last full paragraph on page 37 with the following paragraph:

In this example, a proteomics-derived step was used in order to analyse the expression level of a set of proteins. First, a 2-D ~~Gelelectrophoresis~~ Gel electrophoresis according to standard protocols (see above) was perfomed for both a prostate cancer cell line and cells derived from a healthy prostate in which a staining with Sypro Ruby dye was used. Then, the resulting gels were scanned using a CCD-camera and the scanned picture were analysed using a computer-based analysis software, e.g. "Imagemaster" (Amersham-Pharmacia) or "Z3" (Compugen).